

In the specification:

Please replace the previously amended paragraph on page 8, lines 22-27, of the specification with the following currently amended paragraph.

Fig. 1 shows the sequence alignment of previously known bacterial RNase P protein subunits using the ClustalW alignment program (Thompson et al., Nucleic Acids Research 22: 4673, 1994) and the alignment of the RNase P sequences of the present invention (SEQ ID NOs: 39-95 91).

Please replace the paragraph on page 9, lines 1-23, of the specification with the following amended paragraph.

Figs. 2A-2S shows the nucleic acid sequences (SEQ ID NOs 1-19) encoding the amino acid sequences (SEQ ID NOs 20-38) of the bacterial RNase P polypeptides of the invention. The nucleic acid and amino acid sequences were derived from the following pathogenic bacterial species: *Streptococcus mutans* (Fig. 2A; SEQ ID NOs: 1 and 18 20, respectively); *Klebsiella pneumoniae* (Fig. 2B; SEQ ID NOs: 2 and 19 21, respectively); *Salmonella paratyphi A* (Fig. 2C; SEQ ID NOs: 3 and 20 22, respectively); *Pseudomonas aeruginosa* (Fig. 2D; SEQ ID NOs: 4 and 24 23, respectively); *Corynebacterium diphtheriae* (Fig. 2E; SEQ ID NOs: 5 and 22 24, respectively); *Chlamydia trachomatis* (Fig. 2F; SEQ ID NOs: 6 and 23 25, respectively); *Vibrio cholerae* Serotype 01, Biotype El Tor, Strain N16961 (Fig. 2G; SEQ ID NOs: 7 and 24 26, respectively); *Neisseria gonorrhoea* FA 1090 (Fig. 2H; SEQ ID NOs: 8 and 25 27, respectively); *Neisseria meningitidis* Serogroup A, Strain Z2491 (Fig. 2I; SEQ ID NOs: 9 and 26 28, respectively); *Streptococcus pyogenes* M1 (Fig. 2J; SEQ ID NOs: 10 and 27 29, respectively); *Bordetella pertussis* Tohama I (Fig. 2K; SEQ ID NOs: 11 and 28 30, respectively); *Porphyromonas gingivalis* W83 (Fig. 2L; SEQ ID NOs: 12 and 29 31, respectively); *Streptococcus pneumoniae* Type 4 (Fig. 2M; SEQ ID NOs: 13 and 30 32, respectively); *Clostridium difficile* 630 (Fig. 2N; SEQ ID NOs: 14 and 31 33, respectively); *Camphylobacter jejuni* NCTC (Fig. 2O; SEQ ID NOs: 15 and 32 34, respectively); *Bacillus anthracis* Ames (Fig. 2P; SEQ ID NOs: 16 and 33 35, respectively); *Mycobacterium avium* 104 (Fig. 2Q; SEQ ID NOs: 17 and 34 36, respectively); *Staphylococcus aureus* NCTC

8325 (Fig. 2R; SEQ ID NOs: 18 and 35 37, respectively); and *Staplylococcus aureus* COL (Fig. 2S; SEQ ID NOs: 19 and 36 38, respectively).

Please replace the paragraph on page 22, lines 10-21, of the specification with the following amended paragraph.

The preferred reaction buffer contains 50 mM Tris-HCl (pH 7.5), 100 mM ammonium chloride and 10 mM magnesium chloride. Concentrations of 10-100 mM, 25-500 mM and 1-100 mM of the above, respectively, can be substituted, as can other buffering agents such as MOPS or HEPES, or other monovalent cations, such as sodium or potassium. When the assay is run in either 96 98 or 384-well polystyrene or polypropylene assay plates, there is a very significant decrease in the fluorescence intensity and polarization of the annealed substrate over time in the absence of enzyme. Various conditions have been tested to prevent the loss of signal with time. The preferred conditions include addition of 10-40 µg/ml carbonic anhydrase and 10-100 µg/ml polyC to the buffer. Other materials, such as, 0.5-5% glycerol, 10-100 µg/ml hen egg lysozyme, 10-50 µg/mL tRNA, 1-10 mM DTT, or 2-10 mM DTT can also be added to the buffer to prevent some loss of signal.

Kindly replace the Sequence Listing filed on January 10, 2003, with the amended Sequence Listing, submitted herewith.